



Fida 1 – The Ultimate Biophysics Platform

INSTANT READ-OUTS IN MINUTES

1. Structural integrity

- Sensitivity of 5% variation in size measured as hydrodynamic radius (Rh). Gives insight to folding/unfolding and conformational changes.
- Validate your protein integrity across buffers/matrices.

2. Aggregation

- Protein/particle aggregates are clearly detectable and quantifiable whilst still leaving the core signal useful for standard measurement.

3. Labelling efficiency

- Option of measuring size of up to 3 species in solution. Will e.g., reveal the labelling efficiency of your molecule when you chose the Fida 1 for labelled assays.

4. Functionality/Binding

- Rapid assessment of binding events. Full binding curves and equilibrium Kd's are obtained by loading the autosampler with your titrations.

5. Polydispersity Index (PDI)

- The option of checking monodispersity is an integrated option on all Fida 1 data you generate.

6. Viscosity

- Every measurement also includes detailed information of viscosity.

7. Stickiness

- The shape of the core signal will reveal any stickiness of your binding partners or your binding complexes. Again, the core signal will be useful for standard measurement despite of the stickiness.

IN-DEPTH CUTTING-EDGE APPLICATIONS

- **In-solution validation of structural information – PDB correlator**
 - The Fida 1 readout (Rh) is directly linked to protein structure and provides an absolute measure in nanometers. On this basis, the Fida 1 software includes a PDB correlator for direct comparison of measured in-solution/native conditions Rh and structures obtained from X-ray/Cryo-EM/NMR/AlphaFold.
- **Membrane Proteins**
 - Detergent screening using minimal sample in a rapid automated assay.
 - Binding assays with unpurified membrane preps.
 - Particularly for crude membrane preps, it is significant that Fida 1 enables you to keep your samples at 5°C in the autosampler whilst performing your actual measurement at room-temperature/37°C.
- **Complex interactions**
 - Bi-/Multi-specifics
 - Assessment of multiple Kd's in complex binding events.
 - Option of deconvoluting multi-complex binding events.
 - Protacs/Molecular glues
 - Ternary complex formation in buffer and in cell lysate.
 - Assessment of individual Kd's in the ternary complex.
 - Assessment of "fraction bound" of your Protein-of-Interest.
 - Ubiquitination assay.
 - Stoichiometry/Oligomeric state
 - Absolute read-out in nanometers facilitates reliable insights into stoichiometry of binding events.
 - Liquid-liquid phase separation
 - Phase diagrams.
 - Dilute-phase concentration.
 - Kd of LLPS modulating components.
 - Relative droplet size distribution.
 - Droplet to amyloid transition.
- **Quantification**
 - Biomarkers in plasma/serum/cell lysate.
 - Auto-antibody detection in plasma/serum.
 - Bioprocessing - Therapeutic proteins in fermentation media.
 - Nanoparticles in plasma/serum/fermentation media.

- **Particle characterization**
 - Particle size.
 - Polydispersity index.
 - Aggregation.
- **Clone selection**
 - Clone selection based on information not only on titer but also on affinity. Both parameters can be obtained simultaneously, without purification of the cell supernatant/cell lysate.

TECHNOLOGY CHARACTERISTICS

- **In-solution biophysical characterization**
- **Measurements**
 - Size, Hydrodynamic radius (Rh)
 - “First Principle” measurement of hydrodynamic radius (Rh) in nanometers
 - Range: 0,5 nm – 500 nm Rh
 - Binding Related Intensity Change (BRIC)
 - In parallel with size measurement, an orthogonal BRIC signal is obtained for all measurements
- **Fluorescence detection**
 - Labelled assays with 480nm or 647nm LED detector
 - Label free assays with 280nm LED detector
- **Minimal sample consumption**
 - nL – μ L range
- **Walk-away automation**
 - 100 vial or 2x 96 well plates
- **Temperature controls**
 - Measurement chamber (10-55°C)
 - Autosampler position 1 (4-55°C)
 - Autosampler position 2 (4-55°C)